

- 1 -

SEQUENCE LISTING

<110> Melbourne Health
 Jane , Stephen (US Only)
 Wilanowski, Tomasz (US only)
 Ting, Stephen (US only)

<120> Diagnostic and Therapeutic Agents

<130> 12301370/EJH

<150> US 60/402055

<151> 2002-08-09

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<151> 2002-08-22

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<170> PatentIn version 3.1

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 Met Ala Ser Leu Trp Glu Ser
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 ccc cag cag tgt atc atc ctg agc cca ctg agc ggg tgg tgg ttt tcg 162
 Pro Gln Gln Cys Ile Ile Leu Ser Pro Leu Ser Gly Trp Trp Phe Ser
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 atc gga atc tca ata ctg acc agt tca gct ctg gtg ctc aag ccc caa 210
 Ile Gly Ile Ser Ile Leu Thr Ser Ser Ala Leu Val Leu Lys Pro Gln
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 atg ctc aaa ggc gaa ctc cag act cga cct tct cag aga cct tca agg 258
 Met Leu Lys Gly Glu Leu Gln Thr Arg Pro Ser Gln Arg Pro Ser Arg
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 aag gcg ttc agg agg aac aac ttt gaa tat acc cta gaa gct tca aaa 306
 Lys Ala Phe Arg Arg Asn Asn Phe Glu Tyr Thr Leu Glu Ala Ser Lys
 60 65 70
 tca ctt cga cag aag cca gga gac agt acc atg acg tac ctg aac aaa 354
 Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr Tyr Leu Asn Lys

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75	80	85	
ggc cag ttc tat ccc atc acc ttg aag gag gtg agc agc agt gaa gga			402
Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser Ser Ser Glu Gly			
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atc cat cat ccc atc agc aaa gtt cga agt gtg atc atg gtg gtt ttt			450
Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val Val Phe			
105	110	115	
gct gaa gac aaa agc aga gaa gat cag tta agg cat tgg aag tac tgg			498
Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys Tyr Trp			
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cac tcc cgg cag cac acc gct aaa caa aga tgc att gac ata gct gac			546
His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile Ala Asp			
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tat aaa gaa agc ttc aac act atc agt aac atc gag gag att gcg tat			594
Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile Ala Tyr			
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aac gcc att tcc ttc aca tgg gac atc aac gat gaa gca aag gtt ttc			642
Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys Val Phe			
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atc tct gtg aac tgc tta agc aca gat ttc tct tcc cag aag gga gtg			690
Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val			
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aag ggg ttg cct ctt aac att caa gtt gat acc tat agt tac aac aac			738
Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr Ser Tyr Asn Asn			
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cgc agc aac aag cct gtg cac cgg gcc tac tgc cag atc aag gtc ttc			786
Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys Val Phe			
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tgt gac aag gga gct gag cgg aaa atc agg gat gaa gaa cga aag caa			834
Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln			
235	240	245	
agc aaa aga aaa gtt tct gat gtt aaa gtg cca ctg ctt ccc tct cac			882
Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu Leu Pro Ser His			
250	255	260	
aag cga atg gat atc aca gtt ttc aaa ccc ttc att gat ctc gat act			930
Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile Asp Leu Asp Thr			
265	270	275	
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Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg			
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ggc act cat gtc ctt ccc att gcc tct gaa gaa ttg gag ggt gaa ggc			1026
Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu Glu Gly Glu Gly			
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Ser	Val	Leu	Lys	Arg	Gly	Pro	Tyr	Gly	Thr	Glu	Asp	Asp	Phe	Ala	Val	
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ctc tac gtt cga aag gag tca gaa gaa gtc ttt gat gcc ctg atg ctc      1170
Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu Met Leu
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Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp Lys Tyr
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gat gtt ccc cat gac aag att ggg aaa ata ttc aag aag tgt aaa aag 1266
Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys Lys Lys
380 385 390

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Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr Ser Asn
395 400 405

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Glu Asp Thr
410

tcaccctgac ggagatctaa aggcctgcgg gccacagctc cccaggagtt cagtgcaggt 1423

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Ala Leu Val Leu Lys Pro Gln Met Leu Lys Gly Glu Leu Gln Thr Arg
 35 40 45

Pro Ser Gln Arg Pro Ser Arg Lys Ala Phe Arg Arg Asn Asn Phe Glu
 50 55 60

Tyr Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser
 65 70 75 80

Thr Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys
 85 90 95

Glu Val Ser Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg
 100 105 110

Ser Val Ile Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln
 115 120 125

Leu Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln
 130 135 140

Arg Cys Ile Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser
 145 150 155 160

Asn Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile
 165 170 175

Asn Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp
 180 185 190

Phe Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val
 195 200 205

Asp Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala
 210 215 220

Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile
 225 230 235 240

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Arg Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys
 245 250 255

Val Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys
 260 265 270

Pro Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val
 275 280 285

His Phe Ala Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser
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Glu Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly
 305 310 315 320

Thr Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile
 325 330 335

Glu Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu
 340 345 350

Val Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met
 355 360 365

Glu Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys
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Ile Val Lys His Tyr Ser Asn Glu Asp Thr
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Gln Asn Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp	
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gag gcc tgg aaa tcc ttc ctg gaa aac cct ctc act gca gcg acc aaa	144
Glu Ala Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys	
35 40 45	
gcg atg atg agc atc aat gga gat gaa gac agc gcc gct gcg ctg ggc	192
Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly	
50 55 60	
ctg ctc tat gac tac tac aag gtt cca aga gag aga agg tca tca aca	240
Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr	
65 70 75	
gca aag cca gag gtg gag cac cct gag cca gat cac agc aaa aga aac	288
Ala Lys Pro Glu Val Glu His Pro Glu Pro Asp His Ser Lys Arg Asn	
80 85 90	
agc ata cca att gtg aca gag cag ccc ctc atc tct gct gga gaa aac	336
Ser Ile Pro Ile Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn	
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aga gtg caa gta ctg aaa aat gtg cca ttt aac att gtc ctt ccc cat	384
Arg Val Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His	
115 120 125	
ggc aac cag ctg ggc att gat aag aga ggc cat ctg aca gct tca gat	432
Gly Asn Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Ser Asp	
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acg aca gtc act gtc tcc ata gca acg atg cct acc cac tcc atc aag	480
Thr Thr Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys	
145 150 155	
aca gaa acc cag cca cat ggc ttc gct gtg gga atc ccc cca gca gtg	528
Thr Glu Thr Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val	
160 165 170	
tat cat cct gag ccc act gag cgg gtg gtg gtt ttc gat cgg aay ctc	576
Tyr His Pro Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Asn Leu	
175 180 185 190	
aat act gac cag ttc agc tct ggt gct caa gcc cca aat gct caa agg	624
Asn Thr Asp Gln Phe Ser Ser Gly Ala Gln Ala Pro Asn Ala Gln Arg	
195 200 205	
cga act cca gac tcg acc ttc tca gag acc ttc aag gaa ggc gtt cag	672
Arg Thr Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln	
210 215 220	
gag gtt ttc ttc ccc tcg gat ctc agt ctg cgg atg cct ggc atg aat	720

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Glu Val Phe Phe Pro Ser Asp Leu Ser Leu Arg Met Pro Gly Met Asn	
225 230 235	
tca gag gac tat gtt ttt gac agt gtt tct ggg aac aac ttt gaa tat	768
Ser Glu Asp Tyr Val Phe Asp Ser Val Ser Gly Asn Asn Phe Glu Tyr	
240 245 250	
acc cta gaa gct tca aaa tca ctt cga cag aag cca gga gac agt acc	816
Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr	
255 260 265 270	
atg acg tac ctg aac aaa ggc cag ttc tat ccc atc acc ttg aag gag	864
Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu	
275 280 285	
gtg agc agc agt gaa gga atc cat cat ccc atc agc aaa gtt cga agt	912
Val Ser Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser	
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Val Ile Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu	
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agg cat tgg aag tac tgg cac tcc cgg cag cac acc gct aaa caa aga	1008
Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg	
320 325 330	
tgc att gac ata gct gac tat awa gaa agc ttc aac act atc agt aac	1056
Cys Ile Asp Ile Ala Asp Tyr Xaa Glu Ser Phe Asn Thr Ile Ser Asn	
335 340 345 350	
atc gag gag att gcg tat aac gcc att tcc ttc aca tgg gac atc aac	1104
Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn	
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gat gaa gca aag gtt ttc atc tct gtg aac tgc tta agc aca gat ttc	1152
Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe	
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Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val Asp	
385 390 395	
acc tat agt tac aac aac cgc agc aac aag cct gtg cac cgg gcc tac	1248
Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr	
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tgc cag atc aag gtc ttc tgt gac aag gga gct gag cgg aaa atc agg	1296
Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg	
415 420 425 430	
gat gaa gaa cga aag caa agc aaa aga aaa gtt tct gat gtt aaa gtg	1344
Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val	
435 440 445	
cca ctg ctt ccc tct cac aag cga atg gat atc aca gtt ttc aaa ccc	1392
Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys Pro	

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Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His			
465	470	475	
ttt gcc aac ttg cag cgg ggc act cat gtc ctt ccc att gcc tct gaa			1488
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gaa ttg gag ggt gaa ggc tct gtc ttg aaa agg ggg ccg tac ggc aca			1536
Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr			
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gaa gat gac ttt gct gtc cct cct tct acc aag ctg gcc cgg ata gaa			1584
Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu			
515	520	525	
gaa cca aag aga gtg ctg ctc tac gtt cga aag gag tca gaa gaa gtc			1632
Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val			
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ttt gat gcc ctg atg ctc aaa acc cca tct ttg aag ggc ttg atg gaa			1680
Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu			
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Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile			
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Phe Lys Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile			
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Val Lys His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu			
595	600	605	
gcc ggg ggg tct tac aag ctc acc ctg acg gag atc taaaggcctg			1870
Ala Gly Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile			
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gcaggtaacc ccagtcagcc atgtcgccag cacagggtcta tgtcgaggga atgggttcct			1990
tgcagggttg aggcggggct gcatctggct tgggtggtagc atttaatatc ttgcattggt			2050
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gatttaaagt gaaaacttta ttccaagagt taacagagtc tctgggaagc tttaggacat			2170
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2361

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Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met
 35 40 45

Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly Leu Leu
 50 55 60

Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr Ala Lys
 65 70 75 80

Pro Glu Val Glu His Pro Glu Pro Asp His Ser Lys Arg Asn Ser Ile
 85 90 95

Pro Ile Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val
 100 105 110

Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Gly Asn
 115 120 125

Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Ser Asp Thr Thr
 130 135 140

Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu
 145 150 155 160

Thr Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His

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165	170	175
Pro Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Asn Leu Asn Thr		
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Asp Gln Phe Ser Ser Gly Ala Gln Ala Pro Asn Ala Gln Arg Arg Thr		
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Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val		
210	215	220
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225	230	235 240
Asp Tyr Val Phe Asp Ser Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu		
245	250	255
Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr		
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Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser		
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Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile		
290	295	300
Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His		
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Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile		
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Asp Ile Ala Asp Tyr Xaa Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu		
340	345	350
Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu		
355	360	365
Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser		
370	375	380
Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr		
385	390	395 400

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Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln
 405 410 415

Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu
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Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu
 435 440 445

Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile
 450 455 460

Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala
 465 470 475 480

Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu
 485 490 495

Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr Glu Asp
 500 505 510

Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu Glu Pro
 515 520 525

Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp
 530 535 540

Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile
 545 550 555 560

Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys
 565 570 575

Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys
 580 585 590

His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly
 595 600 605

Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile
 610 615

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 Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu
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 gtg ccc atg ccc agt gac cct cca ttc aat acc cga aga gcc tac acc 156
 Val Pro Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr
 15 20 25 30
 agt gag gat gaa gcc tgg aag tca tac ttg gag aat ccc ctg aca gca 204
 Ser Glu Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala
 35 40 45
 gcc acc aag gcc atg atg agc att aat ggt gat gag gac agt gct gct 252
 Ala Thr Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala
 50 55 60
 gcc ctc ggc ctg ctc tat gac tac tac aag gtt cct cga gac aag agg 300
 Ala Leu Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg
 65 70 75
 ctg ctg tct gta agc aaa gca agt gac agc caa gaa gac cag gag aaa 348
 Leu Leu Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys
 80 85 90
 aga aac tgc ctt ggc acc agt gaa gcc cag agt aat ttg agt gga gga 396
 Arg Asn Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly
 95 100 105 110
 gaa aac cga gtg caa gtc cta aag act gtt cca gtg aac ctt tcc cta 444
 Glu Asn Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu
 115 120 125
 aat caa gat cac ctg gag aat tcc aag cgg gaa cag tac agc atc agc 492
 Asn Gln Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser
 130 135 140
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 Phe Pro Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val
 145 150 155
 aaa gct gaa gat ttc aca cca gtt ttc atg gcc cca cct gtg cac tat 588
 Lys Ala Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr

- 13 -

160	165	170	
ccc cgg gga gat ggg gaa gag caa cga gtg gtt atc ttt gaa cag act			636
Pro Arg Gly Asp Gly Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr			
175	180	185	190
cag tat gac gtg ccc tcg ctg gcc acc cac agc gcc tat ctc aaa gac			684
Gln Tyr Asp Val Pro Ser Leu Ala Thr His Ser Ala Tyr Leu Lys Asp			
	195	200	205
gac cag cgc agc act ccg gac agc aca tac agc gag agc ttc aag gac			732
Asp Gln Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp			
	210	215	220
gca gcc aca gag aaa ttt cgg agt gct tca gtt ggg gct gag gag tac			780
Ala Ala Thr Glu Lys Phe Arg Ser Ala Ser Val Gly Ala Glu Glu Tyr			
	225	230	235
atg tat gat cag aca tca agt ggc aca ttt cag tac acc ctg gaa gcc			828
Met Tyr Asp Gln Thr Ser Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala			
	240	245	250
acc aaa tct ctc cgt cag aag cag ggg gag ggc ccc atg acc tac ctc			876
Thr Lys Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu			
255	260	265	270
aac aaa gga cag ttc tat gcc ata aca ctc agc gag acc gga gac aac			924
Asn Lys Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn			
	275	280	285
aaa tgc ttc cga cac ccc atc agc aaa gtc agg agt gtg gtg atg gtg			972
Lys Cys Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val			
	290	295	300
gtc ttc agt gaa gac aaa aac aga gat gaa cag ctc aaa tac tgg aaa			1020
Val Phe Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys			
	305	310	315
tac tgg cac tct cgg cag cat acg gcg aag cag agg gtc ctt gac att			1068
Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile			
	320	325	330
gcc gat tac aag gag agc ttt aat acg att gga aac att gaa gag att			1116
Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile			
335	340	345	350
gca tat aat gct gtt tcc ttt acc tgg gac gtg aat gaa gag gcg aag			1164
Ala Tyr Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys			
	355	360	365
att ttc atc acc gtg aat tgc ttg agc aca gat ttc tcc tcc caa aaa			1212
Ile Phe Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys			
	370	375	380
ggg gtg aaa gga ctt cct ttg atg att cag att gac aca tac agt tat			1260
Gly Val Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr			
	385	390	395

- 14 -

aac aat cgt agc aat aaa ccc att cat aga gct tat tgc cag atc aag Asn Asn Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys 400 405 410	1308
gtc ttc tgt gac aaa gga gca gaa aga aaa atc cga gat gaa gag cgg Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg 415 420 425 430	1356
aag cag aac agg aag aaa ggg aaa ggc cag gcc tcc caa act caa tgc Lys Gln Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Thr Gln Cys 435 440 445	1404
aac agc tcc tct gat ggg aag ttg gct gcc ata cct tta cag aag aag Asn Ser Ser Ser Asp Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys 450 455 460	1452
agt gac atc acc tac ttc aaa acc atg cct gat ctc cac tca cag cca Ser Asp Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro 465 470 475	1500
gtt ctc ttc ata cct gat gtt cac ttt gca aac ctg cag agg acc gga Val Leu Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly 480 485 490	1548
cag gtg tat tac aac acg gat gat gaa cga gaa ggt ggc agt gtc ctt Gln Val Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Gly Ser Val Leu 495 500 505 510	1596
gtt aaa cgg atg ttc cgg ccc atg gaa gag gag ttt ggt cca gtg cct Val Lys Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro 515 520 525	1644
tca aag cag atg aaa gaa gaa ggg aca aag cga gtg ctc ttg tac gtg Ser Lys Gln Met Lys Glu Glu Gly Thr Lys Arg Val Leu Leu Tyr Val 530 535 540	1692
agg aag gag act gac gat gtg ttc gat gca ttg atg ttg aag tct ccc Arg Lys Glu Thr Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro 545 550 555	1740
aca gtg aag ggc ctg atg gaa gcg ata tct gag aaa tat ggg ctg ccc Thr Val Lys Gly Leu Met Glu Ala Ile Ser Glu Lys Tyr Gly Leu Pro 560 565 570	1788
gtg gag aag ata gca aag ctt tac aag aaa agc aaa aaa ggc atc ttg Val Glu Lys Ile Ala Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu 575 580 585 590	1836
gtg aac atg gat gac aac atc atc gag cac tac tcg aac gag gac acc Val Asn Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr 595 600 605	1884
ttc atc ctc aac atg gag agc atg gtg gag ggc ttc aag gtc acg ctc Phe Ile Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Val Thr Leu 610 615 620	1932

- 15 -

atg gaa atc tagccctggg tttggcatcc gcttttgctg gagctctcag	1981
Met Glu Ile	
625	
tgcgttcctc cctgagagag acagaagccc cagccccaga acctggagac ccatctcccc	2041
catctcacia ctgctgttac aagaccgtgc tggggagtgg ggcaagggac aggccccact	2101
gtcgggtgtgc ttggcccatc cactggcacc taccacggag ctgaagcctg agccccctcag	2161
gaagggtgct taggcctgtt ggattcctat ttattgccc ccttttcctg gagcccaggt	2221
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cactggcctt agaggagaca cagacctgga gaccgtttta atggggggtt ttgcctctgt	2701
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gtgaaaccag cctcaggagg gaaactggga gagagaagct gtggtctcct gctacatgcc	3361
ctgggagctg gaagagaaaa acactcccct aaacaatcgc aaaatgatga accatcatgg	3421
gccactgttc tctttgaggg gacaggttta ggggtttgcg ttcgcccttg tgggctgaag	3481
cactagcttt ttggtagcta gacacatcct gcacccaaag gttctctaca aaggcccaga	3541
tttgtttgta aagcatttg actcttacct ggaggccgc tctctaaggg ctctctgcgc	3601

- 16 -

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tcccacctca tctgtccctg agatgcagag caggatggag ggtctgcttc tagctcagct 3661
gtttctcctt gaggttgccg aggaattgaa ttgaatggga cagagggcag gtgctgtggc 3721
caagaagatc tccgagcagc agtgacgggg caccttgctg tgtgtcctct gggcatgtta 3781
acccttctgt ggggccaaag gtttgcacg tggatccagc tgtgtccag tctgtcccct 3841
cctcctccac tctgactgcc acgccccgga ccagcagctt ggggaccctc cagggtacta 3901
atggggctct gttctgagat ggacaaattc agtggttgaa atacatgttg tactatgcac 3961
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gacacaggca acctaccct ctctctccag cctctttatg aaactgtttg tttgccagtc 4141
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tgatgtgtcc gctgtgtatg ttagctgaac tttgatgagc aaaatttctt gagcgaaaca 4381
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tttttttttt ttttaacaaag tctgaactga g 4532

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 <211> 625
 <212> PRT
 <213> human

<400> 6

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Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu Val Pro
1           5           10          15

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Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr Ser Glu
          20           25           30

```

```

Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr
          35           40           45

```

```

Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu
          50           55           60

```


- 17 -

Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu
65 70 75 80

Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys Arg Asn
85 90 95

Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly Glu Asn
100 105 110

Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu Asn Gln
115 120 125

Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser Phe Pro
130 135 140

Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala
145 150 155 160

Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg
165 170 175

Gly Asp Gly Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr
180 185 190

Asp Val Pro Ser Leu Ala Thr His Ser Ala Tyr Leu Lys Asp Asp Gln
195 200 205

Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Ala Ala
210 215 220

Thr Glu Lys Phe Arg Ser Ala Ser Val Gly Ala Glu Glu Tyr Met Tyr
225 230 235 240

Asp Gln Thr Ser Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys
245 250 255

Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys
260 265 270

Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys
275 280 285

Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe

- 18 -

290 295 300
 Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp
 305 310 315 320
 His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile Ala Asp
 325 330 335
 Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile Ala Tyr
 340 345 350
 Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys Ile Phe
 355 360 365
 Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
 370 375 380
 Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr Asn Asn
 385 390 395 400
 Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys Val Phe
 405 410 415
 Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
 420 425 430
 Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Thr Gln Cys Asn Ser
 435 440 445
 Ser Ser Asp Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys Ser Asp
 450 455 460
 Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro Val Leu
 465 470 475 480
 Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly Gln Val
 485 490 495
 Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Gly Ser Val Leu Val Lys
 500 505 510
 Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro Ser Lys
 515 520 525

- 19 -

Gln Met Lys Glu Glu Gly Thr Lys Arg Val Leu Leu Tyr Val Arg Lys
 530 535 540

Glu Thr Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro Thr Val
 545 550 555 560

Lys Gly Leu Met Glu Ala Ile Ser Glu Lys Tyr Gly Leu Pro Val Glu
 565 570 575

Lys Ile Ala Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu Val Asn
 580 585 590

Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile
 595 600 605

Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Val Thr Leu Met Glu
 610 615 620

Ile
 625

<210> 7
 <211> 1870
 <212> DNA
 <213> HUMAN

<220>
 <221> CDS
 <222> (47)..(1867)
 <223>

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 Met Trp Met
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aat tcc att ctt cct att ttt ctt ttc agg tct gtg cgg ctg cta aag 103
 Asn Ser Ile Leu Pro Ile Phe Leu Phe Arg Ser Val Arg Leu Leu Lys
 5 10 15

aac gac cca gtc aac ttg cag aaa ttc tct tac act agt gag gat gag 151
 Asn Asp Pro Val Asn Leu Gln Lys Phe Ser Tyr Thr Ser Glu Asp Glu
 20 25 30 35

gcc tgg aag acg tac cta gaa aac ccg ttg aca gct gcc aca aag gcc 199
 Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala
 40 45 50

- 20 -

atg atg aga gtc aat gga gat gat gac agt gtt gcg gcc ttg agc ttc	247
Met Met Arg Val Asn Gly Asp Asp Asp Ser Val Ala Ala Leu Ser Phe	
55 60 65	
ctc tat gat tac tac atg ggt ccc aag gag aag cgg ata ttg tcc tcc	295
Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile Leu Ser Ser	
70 75 80	
agc act ggg ggc agg aat gac caa gga aag agg tac tac cat ggc atg	343
Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Arg Tyr Tyr His Gly Met	
85 90 95	
gaa tat gag acg gac ctc act ccc ctt gaa agc ccc aca cac ctc atg	391
Glu Tyr Glu Thr Asp Leu Thr Pro Leu Glu Ser Pro Thr His Leu Met	
100 105 110 115	
aaa ytc ctg aca gag aac gtg tct gga acc cca gag tac cca gat ttg	439
Lys Xaa Leu Thr Glu Asn Val Ser Gly Thr Pro Glu Tyr Pro Asp Leu	
120 125 130	
ctc aag aag aat aac ctg atg agc ttg gag ggg gcc ttg ccc acc cct	487
Leu Lys Lys Asn Asn Leu Met Ser Leu Glu Gly Ala Leu Pro Thr Pro	
135 140 145	
ggc aag gca gct ccc ctc cct gca ggc ccc agc aag ctg gag gcc ggc	535
Gly Lys Ala Ala Pro Leu Pro Ala Gly Pro Ser Lys Leu Glu Ala Gly	
150 155 160	
tct gtg gac agc tac ctg tta ccc acy act gat atg tat gat aat ggc	583
Ser Val Asp Ser Tyr Leu Leu Pro Xaa Thr Asp Met Tyr Asp Asn Gly	
165 170 175	
tcc ctc aac tcc ttg ttt gag agc att cat ggg gtg ccg ccc aca cag	631
Ser Leu Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro Pro Thr Gln	
180 185 190 195	
cgc tgg cag cca gac agc acc ttc aaa gat gac cca cag gag tcg atg	679
Arg Trp Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln Glu Ser Met	
200 205 210	
ctc ttc cca gat atc ctg aaa acc tcc ccg gaa ccc cca tgt cca gag	727
Leu Phe Pro Asp Ile Leu Lys Thr Ser Pro Glu Pro Pro Cys Pro Glu	
215 220 225	
gac tac ccc agc ctc aaa agt gac ttt gaa tac acc ctg ggc tcc ccc	775
Asp Tyr Pro Ser Leu Lys Ser Asp Phe Glu Tyr Thr Leu Gly Ser Pro	
230 235 240	
aaa gcc atc cac atc aag tca ggc gag tca ccc atg gcc tac ctc aac	823
Lys Ala Ile His Ile Lys Ser Gly Glu Ser Pro Met Ala Tyr Leu Asn	
245 250 255	
aaa ggc cag ttc tac ccc gtc acc ctg cgg acc cca gca ggt ggc aaa	871
Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala Gly Gly Lys	
260 265 270 275	

- 21 -

ggc ctt gcc ttg tcc tcc aac aaa gtc aag agt gtg gtg atg gtt gtc	919
Gly Leu Ala Leu Ser Ser Asn Lys Val Lys Ser Val Val Met Val Val	
280 285 290	
ttc gac aat gag aag gtc cca gta gag cag ctg cgc ttc tgg aag cac	967
Phe Asp Asn Glu Lys Val Pro Val Glu Gln Leu Arg Phe Trp Lys His	
295 300 305	
tgg cat tcc cgg caa ccc act gcc aag cag cgg gtc att gac gtg gct	1015
Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile Asp Val Ala	
310 315 320	
gac tgc aaa gaa aac ttc aac act gtg gag cac att gag gag gtg gcc	1063
Asp Cys Lys Glu Asn Phe Asn Thr Val Glu His Ile Glu Glu Val Ala	
325 330 335	
tat aat gca ctg tcc ttt gtg tgg aac gtg aat gaa gag gcc aag gtg	1111
Tyr Asn Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu Ala Lys Val	
340 345 350 355	
ttc atc ggc gta aac tgt ctg agc aca gac ttt tcc tca caa aag ggg	1159
Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly	
360 365 370	
gtg aag ggt gtc ccc ctg aac ctg cag att gac acc tat gac tgt ggc	1207
Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr Asp Cys Gly	
375 380 385	
ttg ggc act gag cgc ctg gta cac cgt gct gtc tgc cag atc aag atc	1255
Leu Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln Ile Lys Ile	
390 395 400	
ttc tgt gac aag gga gct gag agg aag atg cgc gat gac gag cgg aag	1303
Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp Glu Arg Lys	
405 410 415	
cag ttc cgg agg aag gtc aag tgc cct gac tcc agc aac agt ggc gtc	1351
Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn Ser Gly Val	
420 425 430 435	
aag ggc tgc ctg ctg tcg ggc ttc agg ggc aat gag acg acc tac ctt	1399
Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr Thr Tyr Leu	
440 445 450	
cgg cca gag act gac ctg gag acg cca ccc gtg ctg ttc atc ccc aat	1447
Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro Val Leu Phe Ile Pro Asn	
455 460 465	
gtg cac ttc tcc agc ctg cag cgc tct gga ggg gca gcc ccc tcg gca	1495
Val His Phe Ser Ser Leu Gln Arg Ser Gly Gly Ala Ala Pro Ser Ala	
470 475 480	
gga ccc agc agc tcc aac agg ctg cct ctg aag cgt acc tgc tcg ccc	1543
Gly Pro Ser Ser Ser Asn Arg Leu Pro Leu Lys Arg Thr Cys Ser Pro	
485 490 495	
ttc act gag gag ttt gag cct ctg ccc tcc aag cag gcc aag gaa ggc	1591

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Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Gly
500                               505                510                515

gac ctt cag aga gtt ctg ctg tat gtg cgg agg gag act gag gag gtg      1639
Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr Glu Glu Val
                               520                525                530

ttt gac gcg ctc atg ttg aag acc cca gac ctg aag ggg ctg agg aat      1687
Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly Leu Arg Asn
                               535                540                545

gcg atc tct gag aag tat ggg ttc cct gaa gag aac att tac aaa gtc      1735
Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu Glu Asn Ile Tyr Lys Val
                               550                555                560

tac aag aaa tgc aag cga gga atc tta gtc aac atg gac aac aac atc      1783
Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp Asn Asn Ile
                               565                570                575

att cag cat tac agc aac cac gtc gcc ttc ctg ctg gac atg ggg gag      1831
Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp Met Gly Glu
580                               585                590                595

ctg gac ggc aaa att cag atc atc ctt aag gag ctg taa      1870
Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
                               600                605

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<210> 8
<211> 607
<212> PRT
<213> HUMAN

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<220>
<221> misc_feature
<222> (117)..(117)
<223> The 'Xaa' at location 117 stands for Leu, or Phe.

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<220>
<221> misc_feature
<222> (172)..(172)
<223> The 'Xaa' at location 172 stands for Thr.

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<400> 8

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Met Trp Met Asn Ser Ile Leu Pro Ile Phe Leu Phe Arg Ser Val Arg
1                               5                10                15

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```

Leu Leu Lys Asn Asp Pro Val Asn Leu Gln Lys Phe Ser Tyr Thr Ser
                20                25                30

```

```

Glu Asp Glu Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala
35                               40                45

```

- 23 -

Thr Lys Ala Met Met Arg Val Asn Gly Asp Asp Asp Ser Val Ala Ala
50 55 60

Leu Ser Phe Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile
65 70 75 80

Leu Ser Ser Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Arg Tyr Tyr
85 90 95

His Gly Met Glu Tyr Glu Thr Asp Leu Thr Pro Leu Glu Ser Pro Thr
100 105 110

His Leu Met Lys Xaa Leu Thr Glu Asn Val Ser Gly Thr Pro Glu Tyr
115 120 125

Pro Asp Leu Leu Lys Lys Asn Asn Leu Met Ser Leu Glu Gly Ala Leu
130 135 140

Pro Thr Pro Gly Lys Ala Ala Pro Leu Pro Ala Gly Pro Ser Lys Leu
145 150 155 160

Glu Ala Gly Ser Val Asp Ser Tyr Leu Leu Pro Xaa Thr Asp Met Tyr
165 170 175

Asp Asn Gly Ser Leu Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro
180 185 190

Pro Thr Gln Arg Trp Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln
195 200 205

Glu Ser Met Leu Phe Pro Asp Ile Leu Lys Thr Ser Pro Glu Pro Pro
210 215 220

Cys Pro Glu Asp Tyr Pro Ser Leu Lys Ser Asp Phe Glu Tyr Thr Leu
225 230 235 240

Gly Ser Pro Lys Ala Ile His Ile Lys Ser Gly Glu Ser Pro Met Ala
245 250 255

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala
260 265 270

Gly Gly Lys Gly Leu Ala Leu Ser Ser Asn Lys Val Lys Ser Val Val

- 24 -

275	280	285
Met Val Val Phe Asp Asn Glu Lys Val Pro Val Glu Gln Leu Arg Phe 290 295 300		
Trp Lys His Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile 305 310 315 320		
Asp Val Ala Asp Cys Lys Glu Asn Phe Asn Thr Val Glu His Ile Glu 325 330 335		
Glu Val Ala Tyr Asn Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu 340 345 350		
Ala Lys Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser 355 360 365		
Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr 370 375 380		
Asp Cys Gly Leu Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln 385 390 395 400		
Ile Lys Ile Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp 405 410 415		
Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn 420 425 430		
Ser Gly Val Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr 435 440 445		
Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro Val Leu Phe 450 455 460		
Ile Pro Asn Val His Phe Ser Ser Leu Gln Arg Ser Gly Gly Ala Ala 465 470 475 480		
Pro Ser Ala Gly Pro Ser Ser Ser Asn Arg Leu Pro Leu Lys Arg Thr 485 490 495		
Cys Ser Pro Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala 500 505 510		

- 25 -

Lys Glu Gly Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr
 515 520 525

Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly
 530 535 540

Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu Glu Asn Ile
 545 550 555 560

Tyr Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp
 565 570 575

Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp
 580 585 590

Met Gly Glu Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
 595 600 605

<210> 9
 <211> 3113
 <212> DNA
 <213> MURINE

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 <222> (2634)..(2634)
 <223> n = any nucleotide

<220>
 <221> misc_feature
 <222> (2968)..(2968)
 <223> n = any nucleotide

<400> 9
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- 26 -

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- 27 -

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 <211> 536
 <212> PRT
 <213> MURINE

<400> 10

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1           5           10           15

```

```

Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val Gln Val
          20           25           30

```

```

Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Ser Asn Gln Leu
          35           40           45

```

```

Gly Ile Asp Lys Arg Gly His Leu Thr Ala Pro Asp Thr Thr Val Thr
          50           55           60

```

- 28 -

Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu Ile Gln
65 70 75 80

Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His Ser Glu
85 90 95

Pro Thr Glu Arg Val Val Val Phe Asp Arg Ser Leu Ser Thr Asp Gln
100 105 110

Phe Ser Ser Gly Thr Gln Pro Pro Asn Ala Gln Arg Arg Thr Pro Asp
115 120 125

Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val Phe Phe
130 135 140

Pro Ser Glu Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu Asp Tyr
145 150 155 160

Val Phe Asp Asn Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu Glu Ala
165 170 175

Ser Lys Ser Leu Arg Gln Lys Gln Gly Asp Ser Thr Met Thr Tyr Leu
180 185 190

Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Lys Glu Gly Ser Ser Asn
195 200 205

Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val
210 215 220

Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys
225 230 235 240

Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile
245 250 255

Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile
260 265 270

Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys
275 280 285

- 29 -

Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys
 290 295 300

Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Ile Asp Thr Tyr Ser Tyr
 305 310 315 320

Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys
 325 330 335

Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg
 340 345 350

Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Gln Leu Leu Pro
 355 360 365

Ser His Lys Arg Thr Asp Ile Thr Val Phe Lys Pro Phe Leu Asp Leu
 370 375 380

Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Thr Asn Leu
 385 390 395 400

Gln Arg Gly Ser His Val Leu Ser Leu Pro Ser Glu Glu Leu Glu Gly
 405 410 415

Glu Gly Ser Val Leu Lys Arg Gly Pro Phe Gly Thr Glu Asp Asp Phe
 420 425 430

Gly Val Pro Pro Pro Ala Lys Leu Thr Arg Thr Glu Glu Pro Lys Arg
 435 440 445

Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu
 450 455 460

Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp
 465 470 475 480

Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys
 485 490 495

Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr
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Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly Gly Ser

- 30 -

515

520

525

Tyr Lys Leu Thr Leu Thr Glu Ile
 530 535

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 <211> 3452
 <212> DNA
 <213> MURINE

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 <223> n = any nucleotide

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 <222> (3307)..(3307)
 <223> n = any nucleotide

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 taccacagc ggcgtccta taccagttag gatgaagcct ggaagtcgtt cctggaaaac 240
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 gcgctggggc tgctctatga ctactacaag gtccccagag agcgccggtc atcagccgta 360
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 aagtcactgc ggcagaagca aggggacagc actatgacat acctgaataa aggccagttc 960

- 31 -

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cactggaagt actggcactc ccgtcagcac acggccaaac agaggtgcat tgacattgct	1140
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<210> 12
<211> 618
<212> PRT
<213> MURINE

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<400> 12

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Met Thr Gln Glu Tyr Asp Asn Lys Arg Pro Val Leu Val Leu Gln Asn
1          5          10          15

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Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp Glu Ala
20          25          30

```

```

Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met
35          40          45

```

```

Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly Leu Leu
50          55          60

```

```

Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Ala Val Lys
65          70          75          80

```

```

Pro Glu Gly Glu His Pro Glu Pro Glu His Ser Lys Arg Asn Ser Ile
85          90          95

```


- 33 -

Pro Asn Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val
 100 105 110

Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Ser Asn
 115 120 125

Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Pro Asp Thr Thr
 130 135 140

Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu
 145 150 155 160

Ile Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His
 165 170 175

Ser Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Ser Leu Ser Thr
 180 185 190

Asp Gln Phe Ser Ser Gly Thr Gln Pro Pro Asn Ala Gln Arg Arg Thr
 195 200 205

Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val
 210 215 220

Phe Phe Pro Ser Glu Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu
 225 230 235 240

Asp Tyr Val Phe Asp Asn Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu
 245 250 255

Glu Ala Ser Lys Ser Leu Arg Gln Lys Gln Gly Asp Ser Thr Met Thr
 260 265 270

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Lys Glu Gly Ser
 275 280 285

Ser Asn Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile
 290 295 300

Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His
 305 310 315 320

- 34 -

Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile
325 330 335

Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu
340 345 350

Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu
355 360 365

Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
370 375 380

Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Ile Asp Thr Tyr
385 390 395 400

Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln
405 410 415

Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu
420 425 430

Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Gln Leu
435 440 445

Leu Pro Ser His Lys Arg Thr Asp Ile Thr Val Phe Lys Pro Phe Leu
450 455 460

Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Thr
465 470 475 480

Asn Leu Gln Arg Gly Ser His Val Leu Ser Leu Pro Ser Glu Glu Leu
485 490 495

Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Phe Gly Thr Glu Asp
500 505 510

Asp Phe Gly Val Pro Pro Pro Ala Lys Leu Thr Arg Thr Glu Glu Pro
515 520 525

Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp
530 535 540

- 35 -

Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile
 545 550 555 560

Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys
 565 570 575

Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys
 580 585 590

His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly
 595 600 605

Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile
 610 615

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 <212> DNA
 <213> murine

<400> 13
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<210> 14
 <211> 625
 <212> PRT
 <213> murine

<400> 14

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Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu Val Pro
1           5           10           15

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Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr Ser Glu
20           25           30

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- 37 -

Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr
 35 40 45

Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu
 50 55 60

Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu
 65 70 75 80

Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Asp Lys Arg Asn
 85 90 95

Cys Leu Gly Thr Ser Glu Ala Gln Ile Asn Leu Ser Gly Gly Glu Asn
 100 105 110

Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Cys Leu Ser Gln
 115 120 125

Asp His Met Glu Asn Ser Lys Arg Glu Gln Tyr Ser Val Ser Ile Thr
 130 135 140

Glu Ser Ser Ala Val Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala
 145 150 155 160

Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg
 165 170 175

Ala Asp Ser Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr
 180 185 190

Asp Leu Pro Ser Ile Ala Ser His Ser Ser Tyr Leu Lys Asp Asp Gln
 195 200 205

Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Gly Ala
 210 215 220

Ser Glu Lys Phe Arg Ser Thr Ser Val Gly Ala Asp Glu Tyr Thr Tyr
 225 230 235 240

Asp Gln Thr Gly Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys
 245 250 255

- 38 -

Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys
 260 265 270

Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys
 275 280 285

Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe
 290 295 300

Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp
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His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile Ala Asp
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Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile Ala Tyr
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Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys Ile Phe
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Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
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Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr Asn Asn
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Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys Val Phe
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Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
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Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Ala Gln Cys Asn Asn
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Ser Ser Asp Gly Lys Met Ala Ala Ile Pro Leu Gln Lys Lys Ser Asp
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Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro Val Leu
 465 470 475 480

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Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly Gln Val
 485 490 495

Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Ser Ser Val Leu Val Lys
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Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Thr Pro Ser Lys
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Gln Ile Lys Glu Glu Asn Val Lys Arg Val Leu Leu Tyr Val Arg Lys
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Glu Asn Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro Thr Val
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Lys Gly Leu Met Glu Ala Leu Ser Glu Lys Tyr Gly Leu Pro Val Glu
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Lys Ile Thr Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu Val Asn
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Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile
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Ile
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Leu Leu Lys Asn Asp Pro Val Ser Phe Gln Lys Phe Pro Tyr Ser Asn
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Glu Asp Glu Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala
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Thr Lys Ala Met Met Arg Val Asn Gly Asp Glu Glu Ser Val Ala Ala
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ctg agc ttc ctc tac gac tac tat atg ggt ccc aag gag aag cgg ata 424
Leu Ser Phe Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile
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Leu Ser Ser Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Lys Phe Tyr
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cac agc atg gac tat gag ccg gat ctt gcc ccc ctc gag agc ccc aca 520
His Ser Met Asp Tyr Glu Pro Asp Leu Ala Pro Leu Glu Ser Pro Thr
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cac ctc atg aaa ttt ttg aca gag aac gtg tct gga agt cca gac tac 568
His Leu Met Lys Phe Leu Thr Glu Asn Val Ser Gly Ser Pro Asp Tyr
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Thr Asp Gln Leu Lys Lys Asn Asn Leu Leu Gly Leu Glu Gly Val Leu
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Pro Thr Pro Gly Lys Thr Asn Thr Val Pro Pro Gly Pro Ser Lys Leu
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Glu Ala Ser Ser Met Asp Ser Tyr Leu Leu Pro Ala Ser Asp Ile Tyr
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gac aat ggc tcc ctc aac tca tta ttt gag agc att cat ggg gtt cca 760
Asp Asn Gly Ser Leu Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro
175 180 185
ccc aca cag cgc tgg cag cca gac agc acc ttc aaa gat gac cca cag 808
Pro Thr Gln Arg Trp Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln

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tgc cca gag gat tat cca ggc ctc aag agt gac ttt gaa tac acc ctg Cys Pro Glu Asp Tyr Pro Gly Leu Lys Ser Asp Phe Glu Tyr Thr Leu 220 225 230 235			904
ggc tcc ccc aaa gcc att cac atc aaa gca ggg gag tca ccc atg gcc Gly Ser Pro Lys Ala Ile His Ile Lys Ala Gly Glu Ser Pro Met Ala 240 245 250			952
tac ctc aac aag ggt cag ttc tac ccc gtc acc cta cgc acc cca gca Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala 255 260 265			1000
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gaa cgg aag cag ttt cga agg aag gtc aag tgc cca gac tcc agt aac Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn 415 420 425			1480

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acc aca tac ttg cgg cca gaa act gac ctg gag acc cag cct gtg ttg Thr Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Gln Pro Val Leu 445 450 455	1576
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att tgc aaa gtc tac aag aaa tgc aag cga ggc atc ctg gtt aac atg Ile Cys Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met 560 565 570	1912
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          20              25              30

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Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met Met
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Arg Val Asn Gly Asp Glu Glu Ser Val Ala Ala Leu Ser Phe Leu Tyr
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Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile Leu Ser Ser Ser Thr
65              70              75              80

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Gly Gly Arg Asn Asp Gln Gly Lys Lys Phe Tyr His Ser Met Asp Tyr
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Glu Pro Asp Leu Ala Pro Leu Glu Ser Pro Thr His Leu Met Lys Phe
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Leu Thr Glu Asn Val Ser Gly Ser Pro Asp Tyr Thr Asp Gln Leu Lys
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Lys Asn Asn Leu Leu Gly Leu Glu Gly Val Leu Pro Thr Pro Gly Lys
 130 135 140

Thr Asn Thr Val Pro Pro Gly Pro Ser Lys Leu Glu Ala Ser Ser Met
 145 150 155 160

Asp Ser Tyr Leu Leu Pro Ala Ser Asp Ile Tyr Asp Asn Gly Ser Leu
 165 170 175

Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro Pro Thr Gln Arg Trp
 180 185 190

Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln Glu Ser Leu Leu Phe
 195 200 205

Pro Asp Ile Leu Lys Thr Ser Pro Asp Pro Pro Cys Pro Glu Asp Tyr
 210 215 220

Pro Gly Leu Lys Ser Asp Phe Glu Tyr Thr Leu Gly Ser Pro Lys Ala
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Ile His Ile Lys Ala Gly Glu Ser Pro Met Ala Tyr Leu Asn Lys Gly
 245 250 255

Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala Gly Gly Lys Gly Leu
 260 265 270

Ala Leu Ser Ser Ser Lys Val Lys Ser Val Val Met Val Val Phe Asp
 275 280 285

Asn Asp Lys Val Pro Val Glu Gln Leu Arg Phe Trp Arg His Trp His
 290 295 300

Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile Asp Val Ala Asp Cys
 305 310 315 320

Lys Glu Asn Phe Asn Thr Val Gln His Ile Glu Glu Val Ala Tyr Asn
 325 330 335

Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu Ala Lys Val Phe Ile

340

345

350

Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr Asp Cys Gly Ala Gly
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Thr Glu Arg Leu Val His Arg Ala Val Cys Gln Ile Lys Ile Phe Cys
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Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp Glu Arg Lys Gln Phe
405 410 415

Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn Asn Ala Gly Ile Lys
420 425 430

Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr Thr Tyr Leu Arg
435 440 445

Pro Glu Thr Asp Leu Glu Thr Gln Pro Val Leu Phe Ile Pro Asn Leu
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His Phe Ser Ser Leu Gln Arg Pro Gly Gly Val Val Pro Ser Ala Gly
465 470 475 480

His Ser Ser Ser Asp Arg Leu Pro Leu Lys Arg Thr Cys Ser Pro Phe
485 495

Ala Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Asp Asp
500 505 510

Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr Glu Glu Val Phe
515 520 525

Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly Leu Arg Asn Ala
530 535 540

Ile Ser Glu Lys Tyr Gly Leu Pro Glu Glu Asn Ile Cys Lys Val Tyr
545 550 555 560

Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp Asn Asn Ile Ile
565 570 575

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Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp Met Gly Glu Leu
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Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
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<212> DNA

<213> drosophila

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 <212> PRT
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<400> 18

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 35 40 45

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
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Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
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Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
 85 90 95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
 100 105 110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
 115 120 125

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His
 130 135 140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
 145 150 155 160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
 165 170 175

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Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
 180 185 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
 195 200 205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
 210 215 220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
 225 230 235 240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
 245 250 255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
 260 265 270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
 275 280 285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
 290 295 300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
 305 310 315 320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
 325 330 335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
 340 345 350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
 355 360 365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
 370 375 380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
 385 390 395 400

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Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
 405 410 415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
 420 425 430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
 435 440 445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
 450 455 460

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 465 470 475 480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
 485 490 495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
 500 505 510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
 515 520 525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
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Pro Gly Ser Val Ile Thr Gln Lys Ser Phe Asp Tyr Thr Glu Leu Cys
 545 550 555 560

Gln Pro Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val
 565 570 575

Asn Ser Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro
 580 585 590

Thr Thr Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg
 595 600 605

Pro Trp His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile
 610 615 620

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Pro Lys Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro
625 630 635 640

Ile Ser Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn
645 650 655

Lys Gly Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu
660 665 670

Lys Pro Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe
675 680 685

Arg Glu Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp
690 695 700

His Ser Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr
705 710 715 720

Lys Asn Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn
725 730 735

Ala Ile Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn
740 745 750

Ile Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
755 760 765

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp Thr
770 775 780

Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys
785 790 795 800

Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala Ala Lys Arg
805 810 815

Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu Leu Tyr His Pro
820 825 830

Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln Asp Phe Ala Lys Pro
835 840 845

Pro Val Leu Phe Ser Pro Ala Glu Asp Met Glu Lys Val Gly Gln Leu

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850 855 860
 Gly Ile Gly Ala Ala Thr Gly Met Thr Phe Asn Pro Leu Ser Asn Gly
 865 870 875 880
 Asn Ser Asn Ser Asn Ser His Ser Ser Leu Gln Ser Phe Tyr Gly His
 885 890 895
 Glu Thr Asp Ser Pro Asp Leu Lys Gly Ala Ser Pro Phe Leu Leu His
 900 905 910
 Gly Gln Lys Val Ala Thr Pro Thr Leu Lys Phe His Asn His Phe Pro
 915 920 925
 Pro Asp Met Gln Thr Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met
 930 935 940
 Leu Thr Ser Thr Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly
 945 950 955 960
 Arg Met Thr Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg Gln
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 Glu Asn Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr Thr
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 Ile Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr
 995 1000 1005
 Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
 1010 1015 1020
 Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile
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 Phe Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val
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 Thr Leu Thr Glu Leu Pro Asn Gln
 1055 1060

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<210> 30
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<400> 30
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<210> 31
<211> 34
<212> DNA

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<213> drosophila dopa decarboxylase promoter

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<210> 32
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 <213> drosophila PCNA promoter

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 <212> DNA
 <213> human

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 <213> Drosophila

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 agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc 360
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caacaagttg	tttcaataag	ccattttcca	tagagcctaa	gtctaaatat	cgtagttata	4140
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cgtagcctat tgtaatccat ttgtatgttt ggcttaagcg ttttacttgt tgaatataaa 4620
gtgtaaaatt atttttgaaa aaaaaaaacc cacacaaaac acaaatcggt tggtctatat 4680
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tgtacac 4747

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<212> PRT
<213> Drosophila

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<400> 35

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Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu
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Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
          20           25           30

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```

Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
          35           40           45

```

```

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
          50           55           60

```

```

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65           70           75           80

```

```

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
          85           90           95

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```

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
          100          105          110

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Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
 115 120 125

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His
 130 135 140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
 145 150 155 160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
 165 170 175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
 180 185 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
 195 200 205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
 210 215 220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
 225 230 235 240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
 245 250 255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
 260 265 270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
 275 280 285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
 290 295 300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
 305 310 315 320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
 325 330 335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile

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340	345	350
Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp 355 360 365		
Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu 370 375 380		
Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val 385 390 395 400		
Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly 405 410 415		
Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln 420 425 430		
Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala 435 440 445		
Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His 450 455 460		
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln 465 470 475 480		
Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala 485 490 495		
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Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg 515 520 525		
Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly 530 535 540		
Pro Gly Ser Val Ile Thr Gln Lys Ser Phe Asp Tyr Thr Glu Leu Cys 545 550 555 560		
Gln Pro Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val 565 570 575		

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Asn Ser Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro
 580 585 590

Thr Thr Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg
 595 600 605

Pro Trp His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile
 610 615 620

Pro Lys Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro
 625 630 635 640

Ile Ser Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn
 645 650 655

Lys Gly Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu
 660 665 670

Lys Pro Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe
 675 680 685

Arg Glu Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp
 690 695 700

His Ser Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr
 705 710 715 720

Lys Asn Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn
 725 730 735

Ala Ile Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn
 740 745 750

Ile Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
 755 760 765

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp Thr
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Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys
 785 790 795 800

Gly	Ala	Glu	Arg	Lys	Thr	Arg	Asp	Glu	Glu	Arg	Arg	Ala	Ala	Lys	Arg		
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Lys	Met	Thr	Ala	Thr	Gly	Arg	Lys	Lys	Leu	Asp	Glu	Leu	Tyr	His	Pro		
			820					825					830				
Val	Thr	Asp	Arg	Ser	Glu	Phe	Tyr	Gly	Met	Gln	Asp	Phe	Ala	Lys	Pro		
		835					840						845				
Pro	Val	Leu	Phe	Ser	Pro	Ala	Glu	Asp	Met	Glu	Lys	Ser	Phe	Tyr	Gly		
	850					855					860						
His	Glu	Thr	Asp	Ser	Pro	Asp	Leu	Lys	Gly	Ala	Ser	Pro	Phe	Leu	Leu		
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His	Gly	Gln	Lys	Val	Ala	Thr	Pro	Thr	Leu	Lys	Phe	His	Asn	His	Phe		
			885						890					895			
Pro	Pro	Asp	Met	Gln	Thr	Asp	Lys	Lys	Asp	His	Ile	Leu	Asp	Gln	Asn		
			900					905					910				
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			980					985					990				
Lys	Ile	Asp	Asp	Asp	Met	Ile	Ser	Phe	Tyr	Cys	Asn	Glu	Asp	Ile	Phe		
	995						1000					1005					
Leu	Leu	Glu	Val	Gln	Gln	Ile	Glu	Asp	Asp	Leu	Tyr	Asp	Val	Thr			
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 1025 1030

<210> 36
 <211> 5650

<212> DNA

<213> Drosophila

<400> 36

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Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
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His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
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Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu

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 Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
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 530 535 540

- 70 -

Pro Gly Ser Val Ile Thr Gln Lys Ile Leu His Val Asp Ala Pro Thr
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- 71 -

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Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe Arg Glu
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Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr Lys Asn
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- 72 -

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Glu Lys Val Gly Gln Leu Gly Ile Gly Ala Ala Thr Gly Met Thr
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Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met Leu Thr Ser Thr

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- 74 -

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 gagactgact cgccggacct gaagggggcc tcaccgttcc tgctccacgg ccagaagggtg 4380
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 gatcacatac tggaccagaa catgttgacc agcacacccc tgaccgactt tggtcgccc 4500
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 <213> Drosophila

<400> 39

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Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
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Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
 35 40 45

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
 50 55 60

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
 65 70 75 80

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
 85 90 95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
 100 105 110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
 115 120 125

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His
 130 135 140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
 145 150 155 160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
 165 170 175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
 180 185 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
 195 200 205

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Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
 210 215 220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
 225 230 235 240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
 245 250 255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
 260 265 270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
 275 280 285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
 290 295 300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
 305 310 315 320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
 325 330 335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
 340 345 350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
 355 360 365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
 370 375 380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
 385 390 395 400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
 405 410 415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
 420 425 430

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Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
 435 440 445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
 450 455 460

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 465 470 475 480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
 485 490 495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
 500 505 510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
 515 520 525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
 530 535 540

Pro Gly Ser Val Ile Thr Gln Lys Ile Leu His Val Asp Ala Pro Thr
 545 550 555 560

Ala Ser Glu Ala Asp Arg Pro Ser Thr Pro Ser Ser Ser Ile Asn Ser
 565 570 575

Thr Glu Asn Thr Glu Ser Asp Ser Gln Ser Val Ser Gly Ser Glu Ser
 580 585 590

Gly Ser Pro Gly Ala Arg Thr Thr Ala Thr Leu Glu Met Tyr Ala Thr
 595 600 605

Thr Gly Gly Thr Gln Ile Tyr Leu Gln Thr Ser His Pro Ser Thr Ala
 610 615 620

Ser Gly Ala Gly Gly Gly Ala Gly Pro Ala Gly Ala Ala Gly Gly Gly
 625 630 635 640

Gly Val Ser Met Gln Ala Gln Ser Pro Ser Pro Gly Pro Tyr Ile Thr
 645 650 655

- 80 -

Ala Asn Asp Tyr Gly Met Tyr Thr Ala Ser Arg Leu Pro Pro Gly Pro
 660 665 670

Pro Pro Thr Ser Thr Thr Thr Phe Ile Ala Glu Pro Ser Tyr Tyr Arg
 675 680 685

Glu Tyr Phe Ala Pro Asp Gly Gln Gly Gly Tyr Val Pro Ala Ser Thr
 690 695 700

Arg Ser Leu Tyr Gly Asp Val Asp Val Ser Val Ser Gln Pro Gly Gly
 705 710 715 720

Val Val Thr Tyr Glu Gly Arg Phe Ala Gly Ser Val Pro Pro Pro Ala
 725 730 735

Thr Thr Thr Val Leu Thr Ser Val His His His Gln Gln Gln Gln
 740 745 750

Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Gln His His Gln
 755 760 765

Gln Gln Gln His His Ser Gln Asp Gly Lys Ser Asn Gly Gly Ala Thr
 770 775 780

Pro Leu Tyr Ala Lys Ala Ile Thr Ala Ala Gly Leu Thr Val Asp Leu
 785 790 795 800

Pro Ser Pro Asp Ser Gly Ile Gly Thr Asp Ala Ile Thr Pro Arg Asp
 805 810 815

Gln Thr Asn Ile Gln Gln Ser Phe Asp Tyr Thr Glu Leu Cys Gln Pro
 820 825 830

Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val Asn Ser
 835 840 845

Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro Thr Thr
 850 855 860

Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg Pro Trp
 865 870 875 880

His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile Pro Lys

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885

890

895

Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro Ile Ser
 900 905 910

Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn Lys Gly
 915 920 925

Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu Lys Pro
 930 935 940

Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe Arg Glu
 945 950 955 960

Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp His Ser
 965 970 975

Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr Lys Asn
 980 985 990

Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn Ala Ile
 995 1000 1005

Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn Ile
 1010 1015 1020

Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
 1025 1030 1035

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp
 1040 1045 1050

Thr Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys
 1055 1060 1065

Asp Lys Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala
 1070 1075 1080

Ala Lys Arg Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu
 1085 1090 1095

Leu Tyr His Pro Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln
 1100 1105 1110

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Asp Phe Ala Lys Pro Pro Val Leu Phe Ser Pro Ala Glu Asp Met
 1115 1120 1125

Glu Lys Val Gly Gln Leu Gly Ile Gly Ala Ala Thr Gly Met Thr
 1130 1135 1140

Phe Asn Pro Leu Ser Asn Gly Asn Ser Asn Ser Asn Ser His Ser
 1145 1150 1155

Ser Leu Gln Ser Phe Tyr Gly His Glu Thr Asp Ser Pro Asp Leu
 1160 1165 1170

Lys Gly Ala Ser Pro Phe Leu Leu His Gly Gln Lys Val Ala Thr
 1175 1180 1185

Pro Thr Leu Lys Phe His Asn His Phe Pro Pro Asp Met Gln Thr
 1190 1195 1200

Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met Leu Thr Ser Thr
 1205 1210 1215

Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly Arg Met Thr
 1220 1225 1230

Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg Gln Glu Asn
 1235 1240 1245

Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr Thr Ile
 1250 1255 1260

Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr
 1265 1270 1275

Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
 1280 1285 1290

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile
 1295 1300 1305

Phe Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val
 1310 1315 1320

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Thr Leu Thr Glu Leu Pro Asn Gln
1325 1330

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<213> murine

<400> 40
ggatcagaag accatgcc

18

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<400> 41
aggctgttag agttggtg

18

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<400> 42
ctgtagccag ctttcato

18

<210> 43
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<400> 43
gctggtgaaa aggacctct

19

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<400> 44
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20

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<400> 45
cacattgaag aggtggc

17

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<210> 46
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<213> MURINE

<400> 46
aagggtgagc aggttcgctt

20